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1646

NOV 27 2001

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/029,042B

DATE: 11/13/2000
 TIME: 12:44:10

TECH CENTER 1600270

Does Not Comply
 Corrected Diskette Needed

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\11132000\I029042B.raw

4 <110> APPLICANT: Kim, Sun-Young
 5 Kim, Kee-Won
 6 Kim, Tae-Han
 7 Hwang, Jeong-Ho
 8 Kim, Seon-Hee
 9 Lee, Sun-Young
 11 <120> TITLE OF INVENTION: Heterologous Protein Production System using Avian Cells
 0 <130> FILE REFERENCE:
 13 <140> CURRENT APPLICATION NUMBER: US 09/029,042B
 15 <141> CURRENT FILING DATE: 1998-05-15
 17 <150> PRIOR APPLICATION NUMBER: PCT/KR96/00145
 19 <151> PRIOR FILING DATE: 1996-08-23
 21 <160> NUMBER OF SEQ ID NOS: 11

ERRORED SEQUENCES

68 <210> SEQ ID NO: 2
 70 <211> LENGTH: 1583
 72 <212> TYPE: DNA
 74 <213> ORGANISM: erythropoietin
 76 <400> SEQUENCE: 2
 78 atgggggtgc acgaatgtcc tgcctggctg tggettctcc tgcctcctgt 50
 79 gtcctcctcc ctgggcctcc cagtcctggg cgcgccacca cgcctcatct 100
 80 gtgacagccg agtctggag aggtacctct tggaggccaa ggaggccgag 150
 81 aatatcacgg tgagaccctc tcccagcac attccacaga actcacgctc 200
 82 agggcttcag ggaactcctc ccagatccag gaacctggca ctgggtttgg 250
 83 ggtggagltg ggaagctaga cactgccccc ctacataaga ataagtcctg 300
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 86 ctgtgtgcat ttcagacggg ctgtgtgtaa cactgcagct tgaatgagaa 450
 87 tatcactgtc ccagacacca aagttaattt ctatgcctgg aagaggatgg 500
 88 aggtgagttc cttttttttt ttttttctt tcttttggag aatctcattt 550
 89 gcgaacctga ttttgatga aaggagaaat gatcgaggga aaggtaaaa 600
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 93 aaaaattagtc aggtgaagtg gtgcattggt gtagtccccc atatttggaa 800
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 95 ctgtgatcac accactgcac tccagcctca gtgacagayl gaggcctgtl 900
 96 ctcaaaaaag aaagaaaaaa agaaaaataa tgagggctgt atggaalacg 950
 97 ttcattatcc attcaatcac tcaatcacat allcatlcat tcaatcatte 1000
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 99 ccactccctg taggtcgggc agcaggccgt agaagctcgg cagggccttg 1100
 100 cctgtctgtc ggaagctgtc ctgcggggcc aggccttgtt ggtcaactct 1150
 101 tcccagccgt gggagccctc gcagctgcat gtggataaag cgtcagtg 1200
 102 ccttcgcagc ctcaaccactc tgcctcgggc tctgggagcc caggtgagta 1250

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103 ggagcggaca cttctgcttg ccctttctgt aagaagggga gaagggtctt 1300
104 gctaaggagt acaggaactg tccgtattcc ttcctttct gtggcactgc 1350
105 aqcgacctcc tgttttctcc ttggcagaag gaagccatct cccctccaga 1400
106 tgcggcctca gctgctccac tccgaacaat cactgctgac actttccgca 1450
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249 <211> LENGTH: 1587
251 <212> TYPE: DNA
253 <213> ORGANISM: erythropoietin
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259 gtgacagccg agtctctggg aggtacctct tggagggcaa ggagggcgag 150
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261 agggcttccg gggaaactct cccagatcc aggaacctgg cacttggttt 250
262 ggggtggagt tgggaaqcta gacactgccc cctacataa gaataagctc 300
263 ggtggcccca aaccatacct ggaactaggg caaggagcaa agccagcaga 350
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265 cgggctgtgt gcatccaga cgggctgtgc tgaacactgc agcttgaatg 450
266 agaatatcac tctcccagac accaaaqttt atttctatgc ctggaagagg 500
267 atggaggtga gttctctttt tttttttttt cctttctttt ggagaatctc 550
268 atttgcagac ctgatttggg atgaaaagga gaatgatcga gggaaaggta 600
269 aaatggagca gcagagatga gctgtcctgg gcgcagaggg tccagctatc 650
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271 ttcagaccac cctaggcagc ctagttagat ccccatctc tacaacattt 750
272 taaaaaaatt agtcaggtya agtgggtgat ggtggtagtc ccagatattt 800
273 ggaagqctga ggcgggagga tgccttgayc ccaqqaattt gaggtgagc 850
274 tgagctgtga tccaccact gcactccagc ctgagtgaca gagtggagcc 900
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277 attcaacaag tcttattgca taactctctt ttgctcagct tgggtgcttg 1050
E--> 278 ggctgctgag gggcaggagg gagaggggtga catgggttca ctgactccca 1100
279 gagtccactc cctgtaggtc gggcagcagg ccgtagaagt ctggcagggc 1150
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281 ctcttcccag ccgtgggagc cctgcaagct gcatgtggat aaagccgtca 1250
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283 agtaggagcg gacacttctg ctgccccttt ctgtaagaag gggagaaggg 1350
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285 ctgcagcgac cactgttttt ctccttggca gaaggaagcc atctcccctc 1450
286 cagatgcggc ctcagctgct ccaactccga caatcactgc tgacacttcc 1500
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407 <210> SEQ ID NO: 10
409 <211> LENGTH: 193
411 <212> TYPE: PRT
413 <213> ORGANISM: erythropoietin gene
415 <400> SEQUENCE: 10
417 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu

"i" is invalid for use
in the sequence, per
Sequence Rules. Use "n"
and replace in 2207-2237
section.

next page

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PATENT APPLICATION: US/09/029,042B

DATE: 11/13/2000
TIME: 12:44:10

Input Set : A:\PTO.txt
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```

418      1          5          10          15
419  Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
420      20          25          30
421  Ile Cys Asp Arg Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
422      35          40          45
423  Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
424      50          55          60
425  Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
426      65          70          75          80
427  Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Glu Gly Leu Ala Leu
428      85          90          95
429  Leu Ser Glu Ser Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
E--> 430      100 100 105 105 110 110
431  Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
E--> 432      115          120          125
433  Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
E--> 434      130          135          140
435  Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
E--> 436      145          150          155          160
437  Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
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439  Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
E--> 440      180          185          190
441  Arg
445 <210> SEQ ID NO: 11
447 <211> LENGTH: 193
449 <212> TYPE: PRT
451 <213> ORGANISM: erythropoietin gene
453 <400> SEQUENCE: 11
455  Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu
456      1          5          10          15
457  Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
458      20          25          30
459  Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
460      35          40          45
461  Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
462      50          55          60
463  Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
464      65          70          75          80
465  Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
466      85          90          95
467  Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
468      100          105          110
469  Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
470      115          120          125
471  Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
472      130          135          140
473  Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
474      145          150          155          160

```

*misaligned
amino acid numbers*

*see item 4
on Enr summary
sheet*

next page

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Input Set : A:\PTO.txt
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475 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
476 165 170 175
477 Arg Gly Glu Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
478 180 185 190
479 Gly
E--> 480 1

*Delete
at end of file*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/029,042B

DATE: 11/13/2000
TIME: 12:44:11

Input Set : A:\PTO.txt

Output Set: N:\CRF3\11132000\I029042B.raw

L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:108 M:254 E: No. of Bases conflict, LENGTH:Input:1583 Counted:1533 SEQ:2
L:108 M:252 E: No. of Seq. differs. <211>LENGTH:Input:1583 Pound:1533 SEQ:2
L:278 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:430 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:480 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11

**RAW SEQUENCE LISTING
ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH

RECEIVED

NOV 27 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/029,042B

Source:

1646

Date Processed by STIC

11/13/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/029,042R

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTD SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.